

A C A A A A C A A A T C A C A G C A T A T G C C

0 12/21 0 11 11 11 11 11 11 11 11 0 11 11 11 11 11 11 11 11

A C A A A A C A A A T C A C A G C A T A T G C C

0 12/21 0 11 11 11 11 11 11 11 11 0 11 11 11 11 11 11 11 11

Fig. 2D1

	1	2	3	4	5	6	7	8	9	10	11	12
R21	C	A	C	A	T	A	A	T	C	A	C	T
R21A	C	A	C	A	T	A	A	T	C	A	C	T
R21B	C	A	C	A	T	A	A	T	C	A	C	T
R21C	C	A	C	A	T	A	A	T	C	A	C	T
R21D	C	A	C	A	T	A	A	T	C	A	C	T
R21E	C	A	C	A	T	A	A	T	C	A	C	T

Fig. 2D2

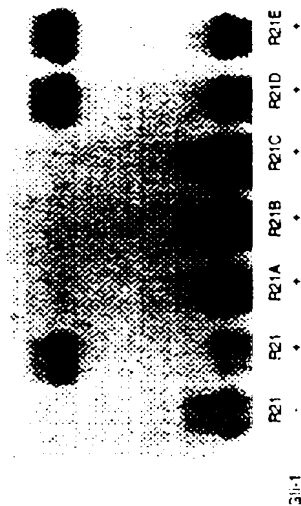


Fig. 2D3

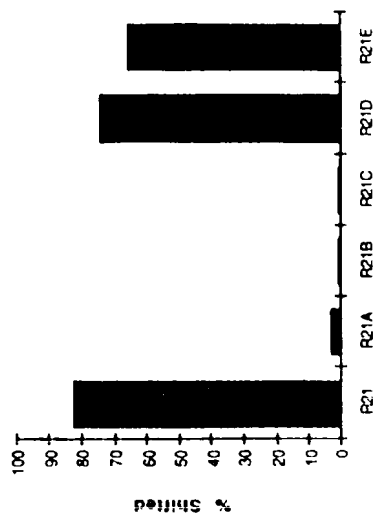


Fig. 2E

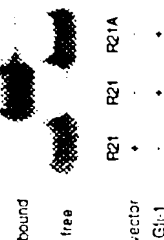


Fig. 2B

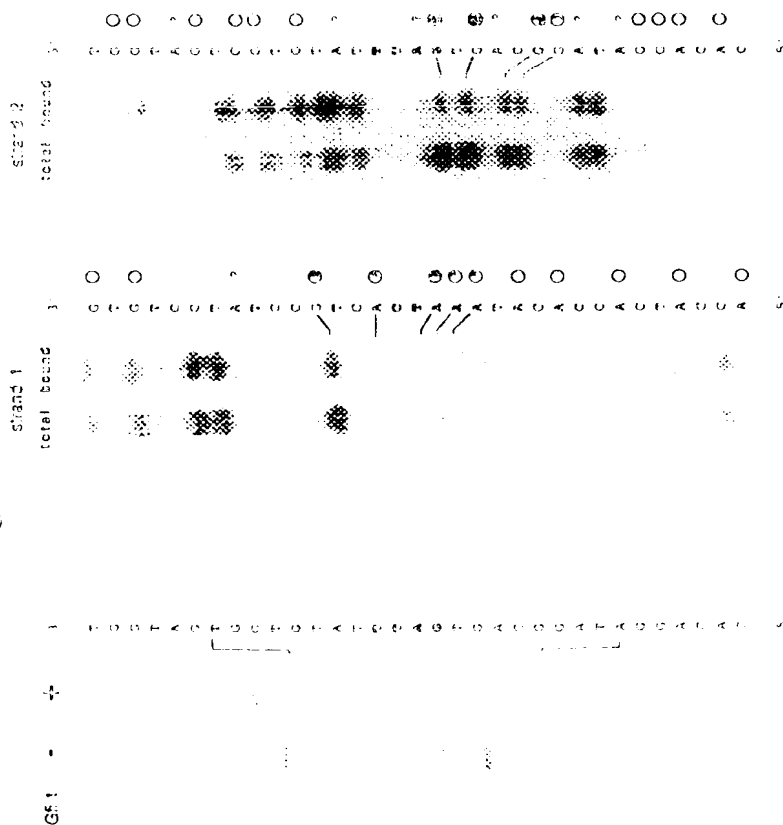


Fig. 2C

1 2 3 4 5 6 7 8 9 10 11 12
 ...ACCATCACCACATATTCACCTGCCTATCCTGIG...
 ...TGGTAGTGGTGTATTAGTGACGGATAGGACAC...
 ...TGGTAGTGGTGTATTAGTGACGGATAGGACAC...

Fig. 3A HCMV MIE Promoter

GCGCGCGCTGGCTGACCGCGCCCAACGACCGCCCGGCCCATTTGACGTCAATAATG
 ACGTATGTTCCCATAGTAACGCCAATAGGGACCTTCCATTGACGTCAATG
 CGTGGAGTATTACGTTAACTGCCCACTTGGCAGTACATCAAGTGATC
 ATATGCCAAAGTACGCCGCCCTATTGACGTCAATGACGGTAAATGCCCCGCC
 TGGCATTATGCCCAAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTA
 CATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTGGCAGT
 ACATCAATGGCGTGGATAGCGGTTTGACTCAGCGGGATTTCGAGTCTC
 CACCGCAATTGACGTCAATGGGAGTTTGTGTTTGGCACCGAAATCAACGGGA
 CTTTCCAAATGTGCTAACAACTCGCGCCCGCCCATTTGACGCAATGGCGGTA
 GCGGTGTACGGTGGGAGGCTCTATATAAGCAGAGCTGTTTAGTGAACCGT

Fig.3B

Gli-1 consensus TAAATCAC²GGCA
 Gli-1 site #1 (-157 to -168) GAAATCCCCGTG
 Gli-1 site #2 (-111 to -100) AAAATCAACGGG

Fig. 3C

Point Mutations
 Wildtype CMV CACGGGGA¹TTTC.....AAATCAACGGG Gli-1 site #1
 Mutant A CACGGGGA¹TTTC.....AAATCAACGGG
 Mutant B CACGGGGA¹TTTC.....AAATCAACGGG Gli-1 site #2

Fig. 3D

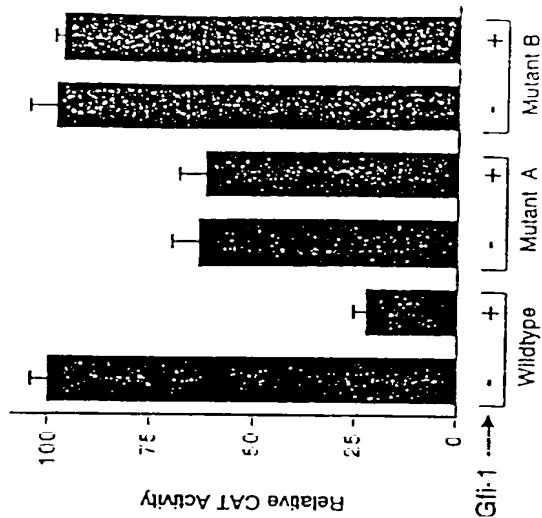


Fig. 4A

	GII-1 aa	Binding Site		3'	5'
		Predicted	R21		
Finger 1	T G V H S Q R T T Q D K Q N T R D R	- X T/C G - A G/t - - A C G/t A A - G/t C G/t	- - - - C... C... G... T... C... A... T... A... T... T... A... - - -	3'	5'
Finger 2					
Finger 3					
Finger 4					
Finger 5					
Finger 6					

Fig. 4B

